

REMARKS

Claims 40-43 and 46-60 are active in the present application.

Applicants wish to thank Examiner Chen and Examiner Foley for the courteous and helpful discussion with their undersigned Representative on November 6, 2003. During this discussion various amendments to address the objection to Claim 41, the indefiniteness rejection, and the anticipation rejection were discussed. Applicants submit that the content of this discussion is reflected in the amendment and remarks set forth herein.

Applicants note that Claim 38 has been canceled and in its place new Claims 57-60 have been presented. Since Claims 57-60 fall within the scope of the previously elected invention, Examination of the same does not constitute a change in the invention and, therefore, new Claims 57-60 should be entered and examined.

Further, Applicants remind the Examiner that MPEP §821.04 states:

...if applicant elects claims directed to the product, and a product claim is subsequently found allowable, withdrawn process claims which depend from or otherwise include all the limitations of the allowable product claim *will be* rejoined.
(*emphasis added*)

Accordingly, Applicants respectfully submit that the non-elected process claims *must* be rejoined following allowance of the elected claims.

The rejection of Claims 38 and 41-43 under 35 U.S.C. §112, second paragraph, is traversed.

The present invention relates to a novel family of human endogenous retroviral sequences (HERV-7q family) that have at least an env domain or motif having the sequence of SEQ ID NO: 1 or a sequence homologous to said sequences (≥80% homology on at least

190 consecutive nucleotides or $\geq 70\%$ homology on at least 600 consecutive nucleotides).

Preferably the endogenous retroviral sequences have an env domain or motif and a gag domain having the sequence of SEQ ID NO: 2 or a sequence homologous to said sequence ($\geq 90\%$ homology on at least 700 consecutive nucleotides or $\geq 70\%$ homology on at least 1200 consecutive nucleotides).

In a particular (and claimed) embodiment, the sequence of the present invention is the HERV-7q sequence (~10.5kb) situated on the long arm of chromosome 7, which corresponds to SEQ ID NO: 3. SEQ ID NO: 3 contains the complete endogenous retroviral sequence: two repeat domains (711 bp, R1 and R2, SEQ ID NO: 20 and 21), delimiting three motifs of the gag type (SEQ ID NO: 2), pol type, and env type (SEQ ID NO: 1). (see Figures 1 and 2).

The env domain corresponds to positions 6965-9550 of SEQ ID NO: 3 (see Figure 1) and has a 2599 bp sequence (SEQ ID NO: 1) which includes an open reading frame of 1620 nucleotides (positions 7874-9493) encoding a protein of 540 amino acids (enverin). SEQ ID NO: 22 (Example 4) contains the enverin open reading frame forms a part of SEQ ID NO: 1.

The gag domain corresponds to positions 3065 to 4390 of SEQ ID NO: 2 (see Figure 1) and has a 1326 bp sequence of SEQ ID NO: 2.

In view of the foregoing explanation, Applicants submit that the metes and bounds of SEQ ID NO: 3 are sufficiently clear. Moreover, Applicants note that this rejection questions the definiteness of a *defined* polynucleotide sequence. Applicants submit that any person of junior high school education has been exposed to and appreciates the clarity, definiteness, and precision that is encompassed by the orchestration and arrangement of the four nucleobases in a polynucleotide sequence. Therefore, with quick reference to the Sequence Listing, the skilled artisan would fully appreciate the exact scope of the claims as presented including all sequences claimed therein.

Withdrawal of this ground of rejection is requested.

The rejection of Claims 38 and 41-43 under 35 U.S.C. §102(b) over Pauley and Waterson is obviated in part by amendment and traversed in part.

It appears that the Examiner has based the rejection over Pauley and Waterson on an interpretation of Claim 38 reading on any sequence in which SEQ ID NO:3 is contained (i.e., chromosomal DNA). However, in view of the present amendment, this interpretation is now believed to be moot.

Pauley and Waterson disclose a 56093 bp fragment from human chromosome 7q21-7q22 comprising 2 genes: the first is located at positions 1360 to 16971 (encodes an ATPase) and the second is located at positions 49698 to 51806 (encodes a protein of unknown function).

The 56093 bp fragment of the human chromosome 7q21-7q22 may contain the HERV-7q sequence (SEQ ID NO: 3) of the invention at positions 28066 to 38281. Further, SEQ ID NO: 1 corresponding to the env domain of HERV-7q matches positions 34954 to 37750 of the 56093 bp fragment of the human chromosome 7q21-7q22 disclosed by Pauley and Waterson. However, Pauley and Waterson specify that the sequence corresponding to positions 21507 to 37303, which lacks part of the HERV-7 sequence, shows similarity to various *ss-RNA virus polyproteins*. At no point do Pauley and Waterson disclose or suggest the HERV-7q sequence (SEQ ID NO: 3), fragment thereof corresponding to the env domain (SEQ ID NO: 1) or the gag domain (SEQ ID NO: 2), or sequences homologous to said env or gag domains, in particular the claimed sequences (SEQ ID NO: 3-8, 10, 13, 16, 17, 20, 21, and 22).

Moreover, Applicants submit that a purified polynucleotide *consisting of* a sequence selected from SEQ ID NO: 3-8, 10, 13, 16, 17, 20, 21, and 22, a complementary sequence thereof, or a reverse complementary sequence thereof would not be obvious in view of the

disclosure by Pauley and Waterson. Specifically, SEQ ID NO: 3 is not obvious in view of Pauley and Waterson, since it is not included but is overlapping partially the region homologous to ss-RNA virus polyproteins specified in Pauley and Waterson. Therefore, this reference fails to ever disclose the claimed sequences with sufficient specificity to justify a conclusion that they were in the public domain in a manner to satisfy the anticipation and/or obviousness standards for examination.

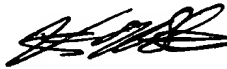
Therefore, Applicants submit that Pauley and Waterson fail to anticipate a purified polynucleotide *consisting of* a sequence selected from SEQ ID NO: 3-8, 10, 13, 16, 17, 20, 21, and 22, a complementary sequence thereof, a reverse complementary sequence thereof, or any fragment thereof. Withdrawal of this ground of rejection is requested.

The objection to Claim 41 is obviated by appropriate amendment. Applicants have deleted the recitation of the term "is", which the Examiner has found objectionable. Applicants request withdrawal of these grounds of objection.

Applicants submit that the present application is in condition for allowance. Early notification to this effect is respectfully requested.

Respectfully submitted,

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